

SEQUENCE LISTING

<110> Chiaur, D.
Pagano, M.
Latres, E.

<120> NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS

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<140> 09/385,219

<141> 1999-08-27

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<151> 1999-02-03

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<170> PatentIn Ver. 2.0

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110

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 Glu Thr Leu Leu Lys Arg Asp Phe Leu Lys Leu Leu Pro Leu Glu Leu
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 Ser Phe Tyr Leu Leu Lys Trp Leu Asp Pro Gln Thr Leu Leu Thr Cys
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 Cys Leu Val Ser Lys Gln Trp Asn Lys Val Ile Ser Ala Cys Thr Glu
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Lys Tyr Leu Pro Leu Leu Asp Arg Ala His Ala Ser Gln Val Cys Arg
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Asn Trp Asn Gln Val Phe His Met Pro Asp Leu Trp Arg Cys Phe Glu
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Phe Glu Leu Asn Gln Pro Ala Thr Ser Tyr Leu Lys Ala Thr His Pro
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Glu Leu Ile Lys Gln Ile Ile Lys Arg His Ser Asn His Leu Gln Tyr
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Val Ser Phe Lys Val Asp Ser Ser Lys Glu Ser Ala Glu Ala Ala Cys
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Asp Ile Leu Ser Gln Leu Val Asn Cys Ser Leu Lys Thr Leu Gly Leu
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Gln	Lys	Tyr	Ser	Leu	Glu	Gln	Ile	His	Trp	Glu	Val	Ser	Lys	His	Leu	405	410		415
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Gln Leu Gly Ser Thr Asn His Tyr Trp Asn Glu Thr Val Arg Asn Pro
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Leu Pro Gly Ala His Gly Thr Glu Phe Pro Asp Pro Lys Val Lys Lys 165 170 175		
Ser Phe Val Thr Ser Tyr Glu Leu Cys Leu Lys Trp Glu Leu Val Asp 180 185 190		
Leu Leu Ala Asp Arg Tyr Trp Glu Glu Leu Leu Asp Thr Phe Arg Pro 195 200 205		
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Ser Leu Ala Thr Ser Ser Asn Gln Thr Ser Ile Gln Asp Glu Gln Pro
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Ser Asp Ser Phe Gln Gly Gln Ala Ala Gln Ser Gly Val Trp Asn Asp
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Thr 180	Glu Ala Lys Ala Leu Ser Leu Pro Glu Lys Trp Lys Leu Ser Gly 190			
Val 195	Tyr Lys Leu Gln Tyr Met His His Leu Cys Glu Gly Ser Ser Ala 205			
Thr 210	Leu Thr Cys Val Pro Leu Gly Asn Leu Ile Val Val Asn Ala Thr 220			
Leu 225	Lys Ile Asn Asn Glu Ile Arg Ser Val Lys Arg Leu Gln Leu Leu 240			
Pro 245	Glu Ser Phe Ile Cys Lys Glu Lys Leu Gly Glu Asn Val Ala Asn 255			
Ile 260	Tyr Lys Asp Leu Gln Lys Leu Ser Arg Leu Phe Lys Asp Gln Leu 270			
Val 275	Tyr Pro Leu Leu Ala Phe Thr Arg Gln Ala Leu Asn Leu Pro Asn 285			
Val 290	Phe Gly Leu Val Val Leu Pro Leu Glu Leu Lys Leu Arg Ile Phe 300			
Arg 305	Leu Leu Asp Val Arg Ser Val Leu Ser Leu Ser Ala Val Cys Arg 320			
Asp 325	Leu Phe Thr Ala Ser Asn Asp Pro Leu Leu Trp Arg Phe Leu Tyr 335			
Leu 340	Arg Asp Phe Arg Asp Asn Thr Val Arg Val Gln Asp Thr Asp Trp 350			
Lys 355	Glu Leu Tyr Arg Lys Arg His Ile Gln Arg Lys Glu Ser Pro Lys 365			
Gly 370	Arg Phe Val Leu Leu Leu Pro Ser Ser Thr His Thr Ile Pro Phe 380			
Tyr 385	Pro Asn Pro Leu His Pro Arg Pro Phe Pro Ser Ser Arg Leu Pro 400			
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Val 420	Gly Asp Pro Ile Ser Ser Leu Ile Pro Gly Pro Gly Glu Thr Pro 430			
Ser 435	Gln Leu Pro Pro Leu Arg Pro Arg Phe Asp Pro Val Gly Pro Leu 445			

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 Ile Gln Thr Leu Gly Leu Ile Ser Thr Ala Lys Pro Ser Phe Met Asn
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 Val Ser Glu Ser His Phe Val Ser Ala Leu Thr Val Val Phe Ile Asn
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 Ser Lys Ser Leu Ser Ser Ile Lys Ile Glu Asp Thr Pro Val Asp Asp
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<210> 26

<211> 634

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> all Xaa positions

<223> Xaa=unknown amino acid residue

<400> 26

Glu Thr Ser Lys Leu Gly Ser Ala Val Leu Ala Pro Ala Ala Gly Gly
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20 25 30
Val Thr Ser Thr Gly Val Asp Lys Ser Leu Asn Gln Leu Leu His Gly
35 40 45
Leu Gly Thr Ser Ser Arg Leu Ser His Phe Pro Phe Gly Lys Ser Pro
50 55 60
Pro Arg Gly Gln Phe Val Ala Ala Ala Val Glu Ile Ala Gly Arg Ser
65 70 75 80
Gly Leu Gln Met Gly Gln Gly Leu Trp Arg Val Val Arg Asn Gln Gln
85 90 95
Leu Gln Gln Glu Gly Tyr Ser Glu Gln Gly Tyr Leu Thr Arg Glu Gln
100 105 110
Ser Arg Arg Met Ala Ala Ser Asn Ile Ser Asn Thr Asn His Arg Lys
115 120 125
Gln Val Gln Gly Gly Ile Asp Ile Tyr His Leu Leu Lys Ala Arg Lys
130 135 140
Ser Lys Glu Gln Glu Gly Phe Ile Asn Leu Glu Met Leu Pro Pro Glu
145 150 155 160
Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr Asp Leu Cys Leu
165 170 175
Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu Leu Leu Trp Gln
180 185 190
Gly Leu Cys Lys Ser Thr Trp Gly His Cys Ser Ile Tyr Asn Lys Asn
195 200 205
Pro Pro Leu Gly Phe Ser Phe Arg Lys Xaa Tyr Met Gln Leu Asp Glu
210 215 220
Gly Ser Leu Thr Phe Asn Ala Asn Pro Asp Glu Gly Val Asn Tyr Phe
225 230 235 240
Met Ser Lys Gly Ile Leu Asp Asp Ser Pro Lys Glu Ile Ala Lys Phe
245 250 255
Ile Phe Cys Thr Arg Thr Leu Asn Trp Lys Lys Leu Arg Ile Tyr Leu
260 265 270
Asp Glu Arg Arg Asp Val Leu Asp Asp Leu Val Thr Leu His Asn Phe
275 280 285
Arg Asn Gln Phe Leu Pro Asn Ala Leu Arg Glu Phe Phe Arg His Ile
290 295 300
His Ala Pro Glu Glu Arg Gly Glu Tyr Leu Glu Thr Leu Ile Thr Lys

305 310 315 320
 Phe Ser His Arg Phe Cys Ala Cys Asn Pro Asp Leu Met Arg Glu Leu
 325 330 335
 Gly Leu Ser Pro Asp Ala Val Tyr Val Leu Cys Tyr Ser Leu Ile Leu
 340 345 350
 Leu Ser Ile Asp Leu Thr Ser Pro His Val Lys Asn Lys Met Ser Lys
 355 360 365
 Arg Glu Phe Ile Arg Asn Thr Arg Arg Ala Ala Gln Asn Ile Ser Glu
 370 375 380
 Asp Phe Val Gly His Leu Tyr Asp Asn Ile Tyr Leu Ile Gly His Val
 385 390 395 400
 Ala Ala Lys Ala Gln Leu Leu Gly Leu Gln Phe Leu Leu Gln Thr Lys
 405 410 415
 Ala Thr Gln Gly Leu Ser Arg Tyr Gly Gly Tyr Ile Ser Ala Gly His
 420 425 430
 Cys Ser Leu Ser Ile Gln Ser Ser Phe Ser Val Gln Pro Phe Phe Leu
 435 440 445
 Leu Pro Phe Ser Ile Leu Val Ile Ser Leu Gly Asn Ile Ile Leu Gln
 450 455 460
 Asn Phe Ser Phe Cys Leu Ser Arg Phe Ala Gln Ser Arg Ala Thr Val
 465 470 475 480
 His Ser Cys Arg Met Ile Asn His Tyr Thr Leu Lys Asp Gly Val Phe
 485 490 495
 Val His Ile Cys Leu Lys Asn Phe Ile His Phe His Ser Leu Tyr Lys
 500 505 510
 Tyr His Val Met Cys Thr Tyr Leu Thr Lys Glu Ile Tyr Ser His Asn
 515 520 525
 Tyr Phe Ile Val Lys Ile Leu Thr Lys Val Phe Pro Phe Leu Ser Asn
 530 535 540
 Val Leu Lys Phe Ile Phe Ser Glu Thr Ile Val Xaa Val Lys Val Arg
 545 550 555 560
 Ser Asp Phe Arg Gln Lys Pro Ile Pro Ala Ser Phe Ser Phe Lys Leu
 565 570 575
 Arg Val Leu Ile Cys Tyr Tyr Ile Thr Met Gln Asn Trp Gln Leu Phe
 580 585 590
 Leu Tyr Lys Phe Ile Ile Phe Phe Ile Leu Lys Thr Gly Leu Ile Lys
 595 600 605
 Ser Arg Val Leu Thr Ile Asp Phe Asn Ile Lys Ile Tyr Asp Leu His
 610 615 620
 Ser Glu Asn Lys Ile Xaa Leu Glu Leu Trp
 625 630

<210> 27
<211> 4168

<212> DNA

<213> Homo sapiens

<400> 27

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gttcttttca	gagcacgttc	cttgtaatgg	cttcagtgac	attgagaacc	ttgaaggacc	420
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<210> 28

<211> 621

<212> PRT

<213> Homo sapiens

<400> 28

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			20					25					30		
Leu	Pro	Gly	Glu	Val	Leu	Glu	Tyr	Ile	Leu	Cys	Cys	Gly	Ser	Leu	Thr
		35					40					45			
Ala	Ala	Asp	Ile	Gly	Arg	Val	Ser	Ser	Thr	Cys	Arg	Arg	Leu	Arg	Glu
	50					55					60				
Leu	Cys	Gln	Ser	Ser	Gly	Lys	Val	Trp	Lys	Glu	Gln	Phe	Arg	Val	Arg
65					70					75					80
Trp	Pro	Ser	Leu	Met	Lys	His	Tyr	Ser	Pro	Thr	Asp	Tyr	Val	Asn	Trp
				85					90					95	
Leu	Glu	Glu	Tyr	Lys	Val	Arg	Gln	Lys	Ala	Gly	Leu	Glu	Ala	Arg	Lys
			100					105					110		
Ile	Val	Ala	Ser	Phe	Ser	Lys	Arg	Phe	Phe	Ser	Glu	His	Val	Pro	Cys
		115					120					125			
Asn	Gly	Phe	Ser	Asp	Ile	Glu	Asn	Leu	Glu	Gly	Pro	Glu	Ile	Phe	Phe
	130					135					140				
Glu	Asp	Glu	Leu	Val	Cys	Ile	Leu	Asn	Met	Glu	Gly	Arg	Lys	Ala	Leu
145					150					155					160
Thr	Trp	Lys	Tyr	Tyr	Ala	Lys	Lys	Ile	Leu	Tyr	Tyr	Leu	Arg	Gln	Gln
				165					170					175	
Lys	Ile	Leu	Asn	Asn	Leu	Lys	Ala	Phe	Leu	Gln	Gln	Pro	Asp	Asp	Tyr
			180					185					190		
Glu	Ser	Tyr	Leu	Glu	Gly	Ala	Val	Tyr	Ile	Asp	Gln	Tyr	Cys	Asn	Pro

Asn Met Asn Val His Ser Leu Pro His Gly His His Gln Pro Phe Tyr
 530 535 540
 Asn Val Leu Val Glu Asp Gly Ser Cys Arg Tyr Ala Ala Gln Glu Asn
 545 550 555 560
 Leu Glu Tyr Asn Val Glu Pro Gln Glu Ile Ser His Pro Asp Val Gly
 565 570 575
 Arg Tyr Phe Ser Glu Phe Thr Gly Thr His Tyr Ile Pro Asn Ala Glu
 580 585 590
 Leu Glu Ile Arg Tyr Pro Glu Asp Leu Glu Phe Val Tyr Glu Thr Val
 595 600 605
 Gln Asn Ile Tyr Ser Ala Lys Lys Glu Asn Ile Asp Glu
 610 615 620

<210> 29
 <211> 278
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> all n positions
 <223> n=a, c, g or t

<400> 29
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 tcccgggntc ctccgtagac ccgcgganac cttcgtgttg agtaacctgg cggaggtggt 120
 ggagcgtgtg ctcaccttcc tgcccgccaa ggcgttgctg cgggtggcct gcgtgtgccg 180
 cttatggagg gagtgtgtgc gcagagtatt gcggacccat cggagcgtaa cctggatctc 240
 cgcaggcctg gcggaggccg gccacctggn ggggcatt 278

<210> 30
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> all Xaa positions
 <223> Xaa=unknown amino acid residue

<400> 30
 Arg Ser Thr Gly Phe Arg Arg Ala Gly Glu Glu Trp Ser Arg Xaa Leu
 1 5 10 15
 Ala Ala Ser Pro Gly Xaa Leu Arg Arg Pro Ala Xaa Thr Phe Val Leu
 20 25 30
 Ser Asn Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala
 35 40 45
 Lys Ala Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys
 50 55 60
 Val Arg Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile Ser Ala

Asp Pro Asn Leu Trp Lys Arg Leu Tyr Met Glu Val Phe Glu Tyr Thr
180 185 190

Arg Pro Met Met His
195

<210> 33
<211> 537
<212> DNA
<213> Homo sapiens

<400> 33
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tggcctcccc ttggagctgt ggcgcatgat cttagcctac ttgcaccttc ccgacctggg 120
ccgctgcagc ctggtatgca gggcctggta tgaactgac ctcagtctcg acagcaccgc 180
ctggcggcag ctgtgtctgg gttgcaccga gtgcgcgcat cccaattggc ccaaccagcc 240
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aggtgaaatc atcttgaagg tgccctgtgga gattgtaggg caggggaagt tgggtga 537

<210> 34
<211> 178
<212> PRT
<213> Homo sapiens

<400> 34
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Met Glu Ala Gly Gly Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala
20 25 30
Tyr Leu His Leu Pro Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala
35 40 45
Trp Tyr Glu Leu Ile Leu Ser Leu Asp Ser Thr Arg Trp Arg Gln Leu
50 55 60
Cys Leu Gly Cys Thr Glu Cys Arg His Pro Asn Trp Pro Asn Gln Pro
65 70 75 80
Asp Val Glu Pro Glu Ser Trp Arg Glu Ala Phe Lys Gln His Tyr Leu
85 90 95
Ala Ser Lys Thr Trp Thr Lys Asn Ala Leu Asp Leu Glu Ser Ser Ile
100 105 110
Cys Phe Ser Leu Phe Arg Arg Arg Arg Glu Arg Arg Thr Leu Ser Val
115 120 125
Gly Pro Gly Arg Glu Phe Asp Ser Leu Gly Ser Ala Leu Ala Met Ala
130 135 140
Ser Leu Tyr Asp Arg Ile Val Leu Phe Pro Gly Val Tyr Glu Glu Gln
145 150 155 160
Gly Glu Ile Ile Leu Lys Val Pro Val Glu Ile Val Gly Gln Gly Lys

165

170

175

Leu Gly

<210> 35

<211> 751

<212> DNA

<213> Homo sapiens

<400> 35

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cagctatcaa gtcgatgatcc gctgtggaga agacattgca aaaaataactg gctgatatact 180
gaggaagaga aaacacagaa gaatcagtggt tggaaatctc tcttcataga tacttactct 240
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<210> 36

<211> 247

<212> PRT

<213> Homo sapiens

<400> 36

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Glu Thr Glu Thr Ala Pro Leu Thr Leu Glu Ser Leu Pro Thr Asp Pro
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      20                      25                      30

Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser Ser His Asp Pro Leu
      35                      40                      45

Trp Arg Arg His Cys Lys Lys Tyr Trp Leu Ile Ser Glu Glu Glu Lys
      50                      55                      60

Thr Gln Lys Asn Gln Cys Trp Lys Ser Leu Phe Ile Asp Thr Tyr Ser
      65                      70                      75                      80

Asp Val Gly Arg Tyr Ile Asp His Tyr Ala Ala Ile Lys Lys Ala Ser
      85                      90                      95

Gly Met Ile Ser Arg Asn Ile Trp Ser Pro Gly Val Leu Gly Trp Val
      100                      105                      110

Leu Ser Leu Lys Glu Gly Cys Ser Arg Gly Arg Pro Arg Cys Cys Gly
      115                      120                      125

Ser Ala Asp Trp Ala Ala Ser Phe Leu Asp Asp Tyr Arg Cys Ser Tyr
      130                      135                      140

Arg Ile His Asn Gly Gln Lys Leu Val Gly Ser Trp Gly Tyr Trp Glu
      145                      150                      155                      160

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Ala Trp His Cys Leu Ile Thr Ile Val Leu Lys Ile Cys Thr Ser Ile
165 170 175

Gln Leu Pro Glu Ile Pro Ala Glu Thr Gly Thr Glu Ile Leu Ser Pro
180 185 190

Phe Asn Phe Cys Ile His Thr Gly Leu Ser Gln Tyr Ile Ala Val Glu
195 200 205

Ala Ala Glu Gly Asn Lys Asn Glu Val Phe Tyr Gln Cys Gln Thr Val
210 215 220

Glu Arg Val Phe Lys Tyr Gly Ile Lys Met Cys Ser Asp Gly Cys Ile
225 230 235 240

Asn Gly Met His Val Phe Ser
245

<210> 37
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 37
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tgggtgctgg gagccctgtt cctggctatc ggctctctgg cctgggggtga gaagggcggt 180
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ctggcaac 368

<210> 38
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> all Xaa positions
<223> Xaa=unknown amino acid residue

<400> 38
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His Gln His Phe Gln Glu Pro Glu Val Gly Cys Cys Gly Lys Tyr Phe
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Leu Phe Gly Phe Asn Ile Val Phe Trp Val Leu Gly Ala Leu Phe Leu
35 40 45

Ala Ile Gly Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile
50 55 60

Ser Ala Leu Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys
65 70 75 80

Gly Ser Trp Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala Ala Ile
85 90 95

Gly Ala Leu Arg Glu Asn Thr Phe Leu Leu Lys Phe Phe Xaa Xaa Phe
100 105 110

Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala
115 120

<210> 39
<211> 774
<212> DNA
<213> Homo sapiens

<400> 39
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gagctggtgg acggcgcccc gctgtggctg ctcaagtgcc agcaggaggg gctggtgccc 180
gagggcgggc tggaggagga gcgcgaccac tggcagcagt tctacttcct gagcaagcgg 240
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accacgatg agagcgtcaa gaagtacttc gcctcctcct ttgagtgggt tgcgaaagca 420
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gccatcgtgg tgaaggactg gtactcgggc cgcagcgacg ctggttgcct ctacgagctc 540
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tacgggcccg gcgtccgctt cgtccgcttc gagcacgggg ggcaggggctc cgtctactgg 720
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<210> 40
<211> 257
<212> PRT
<213> Homo sapiens

<400> 40
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20 25 30

Arg Leu Val Cys Leu Arg Trp Lys Glu Leu Val Asp Gly Ala Pro Leu
35 40 45

Trp Leu Leu Lys Cys Gln Gln Glu Gly Leu Val Pro Glu Gly Gly Val
50 55 60

Glu Glu Glu Arg Asp His Trp Gln Gln Phe Tyr Phe Leu Ser Lys Arg
65 70 75 80

Arg Arg Asn Leu Leu Arg Asn Pro Cys Gly Glu Glu Asp Leu Glu Gly
85 90 95

Trp Cys Asp Val Glu His Gly Gly Asp Gly Trp Arg Val Glu Glu Leu
100 105 110

Pro Gly Asp Ser Gly Val Glu Phe Thr His Asp Glu Ser Val Lys Lys
115 120 125

Tyr Phe Ala Ser Ser Phe Glu Trp Cys Arg Lys Ala Gln Val Ile Asp
130 135 140

Leu Gln Ala Glu Gly Tyr Trp Glu Glu Leu Leu Asp Thr Thr Gln Pro
145 150 155 160

Ala Ile Val Val Lys Asp Trp Tyr Ser Gly Arg Ser Asp Ala Gly Cys
165 170 175

Leu Tyr Glu Leu Thr Val Lys Leu Leu Ser Glu His Glu Asn Val Leu
180 185 190

Ala Glu Phe Ser Ser Gly Gln Val Ala Val Pro Gln Asp Ser Asp Gly
195 200 205

Gly Gly Trp Met Glu Ile Ser His Thr Phe Thr Asp Tyr Gly Pro Gly
210 215 220

Val Arg Phe Val Arg Phe Glu His Gly Gly Gln Gly Ser Val Tyr Trp
225 230 235 240

Lys Gly Trp Phe Gly Ala Arg Val Thr Asn Ser Ser Val Trp Val Glu
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Pro

<210> 41

<211> 957

<212> DNA

<213> Homo sapiens

<400> 41

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<210> 42

<211> 318

<212> PRT

<213> Homo sapiens

<400> 42

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Lys Gly Asn Pro Ile Ser Ile Gln Leu Phe Pro Pro Glu Leu Val Glu	35	40	45
His Ile Ile Ser Phe Leu Pro Val Arg Asp Leu Val Ala Leu Gly Gln	50	55	60
Thr Cys Arg Tyr Phe His Glu Val Cys Asp Gly Glu Gly Val Trp Arg	65	70	75
Arg Ile Cys Arg Arg Leu Ser Pro Arg Leu Gln Asp Gln Asp Thr Lys	85	90	95
Gly Leu Tyr Phe Gln Ala Phe Gly Gly Arg Arg Arg Cys Leu Ser Lys	100	105	110
Ser Val Ala Pro Leu Leu Ala His Gly Tyr Arg Arg Phe Leu Pro Thr	115	120	125
Lys Asp His Val Phe Ile Leu Asp Tyr Val Gly Thr Leu Phe Phe Leu	130	135	140
Lys Asn Ala Leu Val Ser Thr Leu Gly Gln Met Gln Trp Lys Arg Ala	145	150	155
Cys Arg Tyr Val Val Leu Cys Arg Gly Ala Lys Asp Phe Ala Ser Asp	165	170	175
Pro Arg Cys Asp Thr Val Tyr Arg Lys Tyr Leu Tyr Val Leu Ala Thr	180	185	190
Arg Glu Pro Gln Glu Val Val Gly Thr Thr Ser Ser Arg Ala Cys Asp	195	200	205
Cys Val Glu Val Tyr Leu Gln Ser Ser Gly Gln Arg Val Phe Lys Met	210	215	220
Thr Phe His His Ser Met Thr Phe Lys Gln Ile Val Leu Val Gly Gln	225	230	235
Glu Thr Gln Arg Ala Leu Leu Leu Leu Thr Glu Glu Gly Lys Ile Tyr	245	250	255
Ser Leu Val Val Asn Glu Thr Gln Leu Asp Gln Pro Arg Ser Tyr Thr	260	265	270
Val Gln Leu Ala Leu Arg Lys Val Ser His Tyr Leu Pro His Leu Arg	275	280	285
Val Ala Cys Met Thr Ser Asn Gln Ser Ser Thr Leu Tyr Val Thr Asp	290	295	300
Pro Ile Leu Cys Ser Trp Leu Gln Pro Pro Trp Pro Gly Gly	305	310	315

<210> 43

<211> 1590
 <212> DNA
 <213> Homo sapiens

<400> 43
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 gaggaagggg cgagagggcat catcaaagga gatgagggga gcgtaggggc cgggaaagag 240
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<210> 44
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 44
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 Asp Gly Glu Gly Gly Ser Gly Pro Gly Ala Glu Ala Gly Ala Arg Thr
 35 40 45
 Arg Pro Arg Glu Glu Ala Glu Gly Gly Gly Ser Val Glu Glu Gly Ala
 50 55 60
 Arg Gly Ile Ile Lys Gly Asp Glu Gly Ser Val Gly Ala Gly Lys Glu
 65 70 75 80
 Ala Gln Gly Arg Lys Tyr Gly Lys Glu Glu Trp Arg Val Arg Ala Arg
 85 90 95
 Arg Arg Glu Gly Ala Arg Pro Gly Arg Val Gln Gly Gln Gly Gly Gln
 100 105 110
 Val Trp Ala Tyr Ile Pro Gly Thr Gly Ala Ala Met Ala Ala Ala Ala

115						120						125					
Arg	Glu	Glu	Glu	Glu	Glu	Ala	Ala	Arg	Glu	Ser	Ala	Ala	Cys	Pro	Ala		
130						135					140						
Ala	Gly	Pro	Ala	Leu	Trp	Arg	Leu	Pro	Glu	Val	Leu	Leu	Leu	His	Met		
145					150					155					160		
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				165					170					175			
Arg	Trp	Leu	Trp	His	Phe	Thr	Asn	Cys	Asp	Leu	Leu	Arg	Arg	Gln	Ile		
			180					185						190			
Ala	Trp	Ala	Ser	Leu	Asn	Ser	Gly	Phe	Thr	Arg	Leu	Gly	Thr	Asn	Leu		
		195					200					205					
Met	Thr	Ser	Val	Pro	Val	Lys	Val	Ser	Gln	Asn	Trp	Ile	Val	Gly	Cys		
							215					220					
Cys	Arg	Glu	Gly	Ile	Leu	Leu	Lys	Trp	Arg	Cys	Ser	Gln	Met	Pro	Trp		
225					230					235					240		
Met	Gln	Leu	Glu	Asp	Asp	Ala	Leu	Tyr	Ile	Ser	Gln	Ala	Asn	Phe	Ile		
				245					250					255			
Leu	Ala	Tyr	Gln	Phe	Arg	Pro	Asp	Gly	Ala	Ser	Leu	Asn	Arg	Gln	Pro		
			260					265						270			
Leu	Gly	Val	Ser	Ala	Gly	His	Asp	Glu	Asp	Val	Cys	His	Phe	Val	Leu		
		275					280					285					
Ala	Thr	Ser	His	Ile	Val	Ser	Ala	Gly	Gly	Asp	Gly	Lys	Ile	Gly	Leu		
							295					300					
Gly	Lys	Ile	His	Ser	Thr	Phe	Ala	Ala	Lys	Tyr	Trp	Ala	His	Glu	Gln		
305					310					315					320		
Glu	Val	Asn	Cys	Val	Asp	Cys	Lys	Gly	Gly	Ile	Ile	Ser	Phe	Gly	Ser		
				325					330					335			
Arg	Asp	Arg	Thr	Ala	Lys	Val	Trp	Pro	Leu	Ala	Ser	Gly	Gln	Leu	Gly		
			340					345						350			
Gln	Cys	Leu	Tyr	Thr	Ile	Gln	Thr	Glu	Asp	Gln	Ile	Trp	Ser	Val	Ala		
		355					360					365					
Ile	Arg	Pro	Leu	Leu	Ser	Ser	Phe	Val	Thr	Gly	Thr	Ala	Cys	Cys	Gly		
		370					375					380					
His	Phe	Ser	Pro	Leu	Lys	Ile	Trp	Asp	Leu	Asn	Ser	Gly	Gln	Leu	Met		
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Thr	His	Leu	Asp	Arg	Asp	Phe	Pro	Pro	Arg	Ala	Gly	Val	Leu	Asp	Val		
				405					410					415			
Ile	Tyr	Glu	Ser	Pro	Phe	Ala	Leu	Leu	Ser	Cys	Gly	Tyr	Asp	Thr	Tyr		
			420				425						430				
Val	Arg	Tyr	Trp	Asp	Cys	Arg	Thr	Ser	Val	Arg	Lys	Cys	Val	Met	Glu		
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Trp Glu Glu Pro His Asn Ser Thr Leu Tyr Cys Leu Gln Thr Asp Gly
450 455 460

Asn His Leu Leu Ala Thr Gly Ser Ser Phe Tyr Ser Val Val Arg Leu
465 470 475 480

Trp Asp Arg His Gln Arg Ala Cys Pro His Thr Phe Pro Leu Thr Ser
485 490 495

Thr Arg Leu Gly Ser Pro Val Tyr Cys Leu His Leu Thr Thr Lys His
500 505 510

Leu Tyr Ala Ala Leu Ser Tyr Asn Leu His Val Leu Asp Ile Gln Asn
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Pro

<210> 45
<211> 1214
<212> DNA
<213> Homo sapiens

<400> 45
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<210> 46
<211> 272
<212> PRT
<213> Homo sapiens

<400> 46
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Ile Arg Thr Phe Asn Tyr Val Val Lys Leu Leu Gln Leu Ile Ala Lys

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<210> 48
 <211> 483
 <212> PRT
 <213> Homo sapiens

<400> 48

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Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro	35	40	45	
Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly	50	55	60	
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val	65	70	75	80
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala	85	90	95	
Ser	Arg	Pro	Gln	Lys	Glu	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His	100	105	110	
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg	115	120	125	
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg	130	135	140	
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg	145	150	155	160
Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val	165	170	175	
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr	180	185	190	
Asp	Arg	Gly	Leu	Tyr	Thr	Ile	Ala	Gln	Cys	Cys	Pro	Glu	Leu	Arg	Arg	195	200	205	
Leu	Glu	Val	Ser	Gly	Cys	Tyr	Asn	Ile	Ser	Asn	Glu	Ala	Val	Phe	Asp	210	215	220	
Val	Val	Ser	Leu	Cys	Pro	Asn	Leu	Glu	His	Leu	Asp	Val	Ser	Gly	Cys	225	230	235	240
Ser	Lys	Val	Thr	Cys	Ile	Ser	Leu	Thr	Arg	Glu	Ala	Ser	Ile	Lys	Leu	245	250	255	
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Asp	Cys	Phe	Val	Leu	Glu	Asp	Glu	Gly	Leu	His	Thr	Ile	Ala	Ala	His	275	280	285	
Cys	Thr	Gln	Leu	Thr	His	Leu	Tyr	Leu	Arg	Arg	Cys	Val	Arg	Leu	Thr				

290 295 300
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 305 310 315 320
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 325 330 335
 Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys
 340 345 350
 Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser
 355 360 365
 Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His
 370 375 380
 Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp
 385 390 395 400
 Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala
 405 410 415
 Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser
 420 425 430
 Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu
 435 440 445
 Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg
 450 455 460
 Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro
 465 470 475 480
 Ala Phe Phe

<210> 49
 <211> 850
 <212> DNA
 <213> Homo sapiens

<400> 49
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 ggcggaaggc cccatgccct tctggggcag ggctgcgcgc gtgtgccgcc gctggcagga 180
 ggccgcttcc caaccgcgc tctggcacac cgtgaccctg tcgtccccgc tggcggccg 240
 gcctgccaaag ggcggggtca aggcggagaa gaagctcctt gcttccctgg agtggcttat 300
 gcccaatcgg ttttcacagc tccagaggct gacctcatc cactggaagt ctcaggtaca 360
 ccccggtgtg aagctggtag gtgagtgtg tctcggtc actttcctca agctctccgg 420
 ctgccacggt gtgactgtg acgctctggt catgctagcc aaagcctgct gccagctcca 480
 tagcctggac ctacagcact ccatggtgga gtccacagct gtggtgagct tcttgaggga 540
 ggcagggtcc cgaatgcgca agttgtggct gacctacagc tcccagacga cagccatcct 600
 gggcgcatgt ctgggcagct gctgccccca gtgccaggtc ctggaggtga gcaccggcat 660
 caaccgtaat agcattcccc ttcagctgcc tgtcgaggct ctgcagaaag gctgccctca 720
 gctccaggtg ctgcggctgt tgaacctgat gtggctgccc aagcctccgg gacgaggggt 780
 ggctcccga ccaggcttcc ctagcctaga ggagctctgc ctggcgagct caacctgcaa 840
 ctttgtgagc 850

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens
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 Gly Pro Asp Ala Gly Trp Gly Asp Arg Ile Pro Leu Glu Ile Leu Val
 20 25 30
 Gln Ile Phe Gly Leu Leu Val Ala Ala Asp Gly Pro Met Pro Phe Leu
 35 40 45
 Gly Arg Ala Ala Arg Val Cys Arg Arg Trp Gln Glu Ala Ala Ser Gln
 50 55 60
 Pro Ala Leu Trp His Thr Val Thr Leu Ser Ser Pro Leu Val Gly Arg
 65 70 75 80
 Pro Ala Lys Gly Gly Val Lys Ala Glu Lys Lys Leu Leu Ala Ser Leu
 85 90 95
 Glu Trp Leu Met Pro Asn Arg Phe Ser Gln Leu Gln Arg Leu Thr Leu
 100 105 110
 Ile His Trp Lys Ser Gln Val His Pro Val Leu Lys Leu Val Gly Glu
 115 120 125
 Cys Cys Pro Arg Leu Thr Phe Leu Lys Leu Ser Gly Cys His Gly Val
 130 135 140
 Thr Ala Asp Ala Leu Val Met Leu Ala Lys Ala Cys Cys Gln Leu His
 145 150 155 160
 Ser Leu Asp Leu Gln His Ser Met Val Glu Ser Thr Ala Val Val Ser
 165 170 175
 Phe Leu Glu Glu Ala Gly Ser Arg Met Arg Lys Leu Trp Leu Thr Tyr
 180 185 190
 Ser Ser Gln Thr Thr Ala Ile Leu Gly Ala Leu Leu Gly Ser Cys Cys
 195 200 205
 Pro Gln Leu Gln Val Leu Glu Val Ser Thr Gly Ile Asn Arg Asn Ser
 210 215 220
 Ile Pro Leu Gln Leu Pro Val Glu Ala Leu Gln Lys Gly Cys Pro Gln
 225 230 235 240
 Leu Gln Val Leu Arg Leu Leu Asn Leu Met Trp Leu Pro Lys Pro Pro
 245 250 255
 Gly Arg Gly Val Ala Pro Gly Pro Gly Phe Pro Ser Leu Glu Glu Leu
 260 265 270
 Cys Leu Ala Ser Ser Thr Cys Asn Phe Val Ser
 275 280

<210> 51

<211> 1777

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> all n positions

<223> n=a, c, g or t

<400> 51

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agaagtgtca gaacactcca caggataaac ccactcttcc cctgaggtaa tgctgtcaat 180
tttcagctat cttaatcctc aagagttatg tcgatgcagt caagtaagca tgaaatgggtc 240
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atctgaagag tctgcgaggg aatcaattgc tatcagcatt gcacaaatgg aaaaacgttt 480
actccatggc ttaattcata acgttctacc atatgttggg acttctgtaa aaaccttagt 540
attagcatac agctctgcag tttccagcaa aatgggttagg cagatttttag agctttgtcc 600
taacctggag catctggatc ttaccagac tgacatttca gattctgcat ttgacagttg 660
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cacagatgtg gccctagaga agatttccag agctcttgga attctgacat ctcacaaaag 780
tggtctttttg aaaacatcta caagcaaaat tacttcaact gcgtggaaaa ataaagacat 840
taccatgcag tccaccaagc agtatgcctg tttgcacgat ttaactaaca agggcattgg 900
agaagaaata gataatgaac acccctggac taagcctgtt tcttctgaga atttcacttc 960
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catttcttgt gttaaccatc cctttttgag cgtgacttgt tttgggcccc ttnyttacaa 1740
cttcagaaat cttaattacc agtgrattgt aatgttg 1777
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<210> 52

<211> 590

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> all Xaa positions

<223> Xaa=unknown amino acid residue

<400> 52

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  1                      5                      10                      15

Leu Trp Asn His Ala Glu Glu Arg Gln Lys Phe Phe Lys Tyr Ser Val
                20                      25                      30

Asp Glu Lys Ser Asp Lys Glu Ala Glu Val Ser Glu His Ser Thr Gly
  35                      40                      45
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Ile Thr His Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu
 50 55 60
 Asn Pro Gln Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser
 65 70 75 80
 Gln Leu Thr Lys Thr Gly Ser Leu Trp Lys His Leu Tyr Pro Val His
 85 90 95
 Trp Ala Arg Gly Asp Trp Tyr Ser Gly Pro Ala Thr Glu Leu Asp Thr
 100 105 110
 Glu Pro Asp Asp Glu Trp Val Lys Asn Arg Lys Asp Glu Ser Arg Ala
 115 120 125
 Phe His Glu Trp Asp Glu Asp Ala Asp Ile Asp Glu Ser Glu Glu Ser
 130 135 140
 Ala Glu Glu Ser Ile Ala Ile Ser Ile Ala Gln Met Glu Lys Arg Leu
 145 150 155 160
 Leu His Gly Leu Ile His Asn Val Leu Pro Tyr Val Gly Thr Ser Val
 165 170 175
 Lys Thr Leu Val Leu Ala Tyr Ser Ser Ala Val Ser Ser Lys Met Val
 180 185 190
 Arg Gln Ile Leu Glu Leu Cys Pro Asn Leu Glu His Leu Asp Leu Thr
 Gln Thr Asp Ile Ser Asp Ser Ala Phe Asp Ser Trp Ser Trp Leu Gly
 210 215 220
 Cys Cys Gln Ser Leu Arg His Leu Asp Leu Ser Gly Cys Glu Lys Ile
 225 230 235 240
 Thr Asp Val Ala Leu Glu Lys Ile Ser Arg Ala Leu Gly Ile Leu Thr
 245 250 255
 Ser His Gln Ser Gly Phe Leu Lys Thr Ser Thr Ser Lys Ile Thr Ser
 260 265 270
 Thr Ala Trp Lys Asn Lys Asp Ile Thr Met Gln Ser Thr Lys Gln Tyr
 275 280 285
 Ala Cys Leu His Asp Leu Thr Asn Lys Gly Ile Gly Glu Glu Ile Asp
 290 295 300
 Asn Glu His Pro Trp Thr Lys Pro Val Ser Ser Glu Asn Phe Thr Ser
 305 310 315 320
 Pro Tyr Val Trp Met Leu Asp Ala Glu Asp Leu Ala Asp Ile Glu Asp
 325 330 335
 Thr Val Glu Trp Arg His Arg Asn Val Glu Ser Leu Cys Val Met Glu
 340 345 350
 Thr Ala Ser Asn Phe Ser Cys Ser Thr Ser Gly Cys Phe Ser Lys Asp
 355 360 365
 Ile Val Gly Leu Arg Thr Ser Val Cys Trp Gln Gln His Cys Ala Ser
 370 375 380

Pro Ala Phe Ala Tyr Cys Gly His Ser Phe Cys Cys Thr Gly Thr Ala
385 390 395 400

Leu Arg Thr Met Ser Ser Leu Pro Glu Ser Ser Ala Met Cys Arg Lys
405 410 415

Ala Ala Arg Thr Arg Leu Pro Arg Gly Lys Asp Leu Ile Tyr Phe Gly
420 425 430

Ser Glu Lys Ser Asp Gln Glu Thr Gly Arg Val Leu Leu Phe Leu Ser
435 440 445

Leu Ser Gly Cys Tyr Gln Ile Thr Asp His Gly Leu Arg Val Leu Thr
450 455 460

Leu Gly Gly Gly Leu Pro Tyr Leu Glu His Leu Asn Leu Ser Gly Cys
465 470 475 480

Leu Thr Ile Thr Gly Ala Gly Leu Gln Asp Leu Val Ser Ala Cys Pro
485 490 495

Ser Leu Asn Asp Glu Tyr Phe Tyr Tyr Cys Asp Asn Ile Asn Gly Pro
500 505 510

His Ala Asp Thr Ala Ser Gly Cys Gln Asn Leu Gln Cys Gly Phe Arg
515 520 525

Ala Cys Cys Arg Ser Gly Glu Pro Leu Thr Ser Asp Leu Cys Leu Leu
530 535 540

His Leu Ala Glu Gln Ala Phe Phe His Ala Leu Tyr Ser His Ile Ser
545 550 555 560

Cys Val Asn His Pro Phe Leu Ser Val Thr Cys Phe Gly Pro Ile Xaa
565 570 575

Tyr Asn Phe Arg Asn Leu Asn Tyr Gln Xaa Ile Val Met Leu
580 585 590

<210> 53
<211> 1681
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 53
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gagggcaaaa ggagcactag ctaggtcaga gccatgtttc aggtcacaaat gtgatgtcag 180
atggtgctta taaatccttt cttgtcttcg ccattcttaa atcttgatag gtgcctgttg 240
ggaaactgta aatgcctttc ccaatggaga atcaacagat tgggtgatgg tggagtcggt 300
caggaagact caggtcttct agaggaaagg atgcctcatc accccttngg cccaggcagc 360
tgctgtcaga gaatgacaca gcacctgcac agtcgctgtc cacttcctgc cactgctgtc 420
gggtggggtga cgggagcaaa gtaggcgtgg actttgacat gagggagctg agcccgcatc 480
cgcttgatgc ctgcacgggt aacctgctgg cagtcgtaca gctcgaggcg ctccaggcct 540
cggcagttct ctaggtgtyc cagggccaca tcagtgatga ggaggcagtt gtccaactcc 600

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tggtatgagt tgctgtcggt tatcaggatg cawtcttcaa gatccatctt ctccaattcg 780
tggcaattcc gagctaaaag tgtaaaacct gcgtcagtca aatgggagca tcgggcagcc 840
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ccctctacat ctatttgaaa gttaaaaaga tctattcttt gccagttgct tccatccagg 1500
gctaagatgt tccaagcctt ggaaatctgt gcacatcggc acaaagttac tatatccaag 1560
aaggaaaata ttcttaacag aagttctttg ggtaactttt tgtaataaag gccttcatca 1620
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<210> 54
<211> 437
<212> PRT
<213> Homo sapiens

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<220>
<221> SITE
<222> all Xaa positions
<223> Xaa=unknown amino acid residue

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<400> 54
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Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro Lys Glu
      20             25             30

Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu Cys Arg
 35             40             45

Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp Gly Ser
 50             55             60

Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Ile Asp Val Glu Gly
 65             70             75             80

Arg Val Val Glu Asn Ile Ser Lys Arg Cys Val Gly Phe Leu Arg Lys
      85             90             95

Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Asp Ser Ser Leu Lys Thr
 100            105            110

Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn Gly Cys
 115            120            125

Thr Lys Ile Thr Asp Ser Thr Cys Tyr Ser Leu Ser Arg Phe Cys Ser
 130            135            140

Lys Leu Lys His Leu Xaa Leu Thr Ser Cys Val Ser Ile Thr Asn Ser
 145            150            155            160

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Ser Leu Lys Gly Ile Ser Glu Gly Cys Arg Asn Leu Glu Tyr Leu Asn
 165 170 175
 Leu Ser Trp Cys Asp Gln Ile Thr Lys Asp Gly Ile Glu Ala Leu Val
 180 185 190
 Arg Gly Cys Arg Gly Leu Lys Ala Leu Leu Leu Arg Gly Cys Thr Gln
 195 200 205
 Leu Glu Asp Glu Ala Leu Lys His Ile Gln Asn Tyr Cys His Glu Leu
 210 215 220
 Val Ser Leu Asn Leu Gln Ser Cys Ser Arg Ile Thr Asp Glu Gly Val
 225 230 235 240
 Val Gln Ile Cys Arg Gly Cys His Arg Leu Gln Ala Leu Cys Leu Ser
 245 250 255
 Gly Cys Ser Asn Leu Thr Asp Ala Ser Leu Thr Ala Leu Gly Leu Asn
 260 265 270
 Cys Pro Arg Leu Gln Ile Leu Glu Ala Ala Arg Cys Ser His Leu Thr
 275 280 285
 Asp Ala Gly Phe Thr Leu Leu Ala Arg Asn Cys His Glu Leu Glu Lys
 290 295 300
 Met Asp Leu Glu Xaa Cys Ile Leu Ile Thr Asp Ser Thr Leu Ile Gln
 305 310 315 320
 Leu Ser Ile His Cys Pro Lys Leu Gln Ala Leu Ser Leu Ser His Cys
 325 330 335
 Glu Leu Ile Xaa Asp Asp Gly Ile Leu His Leu Ser Asn Ser Thr Cys
 340 345 350
 Gly His Glu Arg Leu Arg Val Leu Glu Leu Asp Asn Cys Leu Leu Ile
 355 360 365
 Thr Asp Val Ala Leu Xaa His Leu Glu Asn Cys Arg Gly Leu Glu Arg
 370 375 380
 Leu Glu Leu Tyr Asp Cys Gln Gln Val Thr Arg Ala Gly Ile Lys Arg
 385 390 395 400
 Met Arg Ala Gln Leu Pro His Val Lys Val His Ala Tyr Phe Ala Pro
 405 410 415
 Val Thr Pro Pro Thr Ala Val Ala Gly Ser Gly Gln Arg Leu Cys Arg
 420 425 430
 Cys Cys Val Ile Leu
 435

<210> 55

<211> 1866

<212> DNA

<213> Homo sapiens

<400> 55

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aacagccaga cttccctct caatgcagag gtatgccagt atgccaaaga agtagtggt 180
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cagtga 1866

<210> 56

<211> 621

<212> PRT

<213> Homo sapiens

<400> 56

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20 25 30

Asn Thr His Arg Ala Ile Glu Ser Asn Ser Gln Thr Ser Pro Leu Asn
35 40 45

Ala Glu Val Val Gln Tyr Ala Lys Glu Val Val Asp Phe Ser Ser His
50 55 60

Tyr Gly Ser Glu Asn Ser Met Ser Tyr Thr Met Trp Asn Leu Ala Gly
65 70 75 80

Val Pro Asn Val Phe Pro Ser Ser Gly Asp Phe Thr Gln Thr Ala Val
85 90 95

Phe Arg Thr Tyr Gly Thr Trp Trp Asp Gln Cys Pro Ser Ala Ser Leu
100 105 110

Pro Phe Lys Arg Thr Pro Pro Asn Phe Gln Ser Gln Asp Tyr Val Glu

115		120		125
Leu Thr Phe Glu Gln Gln Val Tyr Pro Thr Ala Val His Val Leu Glu				
130		135		140
Thr Tyr His Pro Gly Ala Val Ile Arg Ile Leu Ala Cys Ser Ala Asn				
145		150		155
Pro Tyr Ser Pro Asn Pro Pro Ala Glu Val Arg Trp Glu Ile Leu Trp				
		165		170
Ser Glu Arg Pro Thr Lys Val Asn Ala Ser Gln Ala Arg Gln Phe Lys				
		180		185
Pro Cys Ile Lys Gln Ile Asn Phe Pro Thr Asn Leu Ile Arg Leu Glu				
		195		200
Val Asn Ser Ser Leu Leu Glu Tyr Tyr Thr Glu Leu Asp Ala Val Val				
		210		215
Leu His Gly Val Lys Asp Lys Pro Val Leu Ser Leu Lys Thr Ser Leu				
		225		230
Ile Asp Met Asn Asp Ile Glu Asp Asp Ala Tyr Ala Glu Lys Asp Gly				
		245		250
Cys Gly Met Asp Ser Leu Asn Lys Lys Phe Ser Ser Ala Val Leu Gly				
		260		265
Glu Gly Pro Asn Asn Gly Tyr Phe Asp Lys Leu Pro Tyr Glu Leu Ile				
		275		280
Gln Leu Ile Leu Asn His Leu Thr Leu Pro Asp Leu Cys Arg Leu Ala				
		290		295
Gln Thr Cys Lys Leu Leu Ser Gln His Cys Cys Asp Pro Leu Gln Tyr				
		305		310
Ile His Leu Asn Leu Gln Pro Tyr Trp Ala Lys Leu Asp Asp Thr Ser				
		325		330
Leu Glu Phe Leu Gln Ser Arg Cys Thr Leu Val Gln Trp Leu Asn Leu				
		340		345
Ser Trp Thr Gly Asn Arg Gly Phe Ile Ser Val Ala Gly Phe Ser Arg				
		355		360
Phe Leu Lys Val Cys Gly Ser Glu Leu Val Arg Leu Glu Leu Ser Cys				
		370		375
Ser His Phe Leu Asn Glu Thr Cys Leu Glu Val Ile Ser Glu Met Cys				
		385		390
Pro Asn Leu Gln Ala Leu Asn Leu Ser Ser Cys Asp Lys Leu Pro Pro				
		405		410
Gln Ala Phe Asn His Ile Ala Lys Leu Cys Ser Leu Lys Arg Leu Val				
		420		425
Leu Tyr Arg Thr Lys Val Glu Gln Thr Ala Leu Leu Ser Ile Leu Asn				
		435		440
				445

Phe Cys Ser Glu Leu Gln His Leu Ser Leu Gly Ser Cys Val Met Ile
450 455 460
Glu Asp Tyr Asp Val Ile Ala Ser Met Ile Gly Ala Lys Cys Lys Lys
465 470 475 480
Leu Arg Thr Leu Asp Leu Trp Arg Cys Lys Asn Ile Thr Glu Asn Gly
485 490 495
Ile Ala Glu Leu Ala Ser Gly Cys Pro Leu Leu Glu Glu Leu Asp Leu
500 505 510
Gly Trp Cys Pro Thr Leu Gln Ser Ser Thr Gly Cys Phe Thr Arg Leu
515 520 525
Ala His Gln Leu Pro Asn Leu Gln Lys Leu Phe Leu Thr Ala Asn Arg
530 535 540
Ser Val Cys Asp Thr Asp Ile Asp Glu Leu Ala Cys Asn Cys Thr Arg
545 550 555 560
Leu Gln Gln Leu Asp Ile Leu Gly Thr Arg Met Val Ser Pro Ala Ser
565 570 575
Leu Arg Lys Leu Leu Glu Ser Cys Lys Asp Leu Ser Leu Leu Asp Val
580 585 590
Ser Phe Cys Ser Gln Ile Asp Asn Arg Ala Val Leu Glu Leu Asn Ala
595 600 605
Ser Phe Pro Lys Val Phe Ile Lys Lys Ser Phe Thr Gln
610 615 620

<210> 57
<211> 984
<212> DNA
<213> Homo sapiens

<400> 57
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tctacttccc agcagcaact cacatttcag gagtctgtgc ttaaactgtg tcagcctgag 180
cttgagagca gtcagattca catatcagtg ctgccaatgg aggtcctgat gtacatcttc 240
cgatgggtgg tgtctagtga cttggacctc agatcattgg agcagttgtc gctgggtgtgc 300
agaggattct acatctgtgc cagagaccct gaaatatggc gtctggcctg cttgaaagtt 360
tggggcagaa gctgtattaa acttgttccg tacacgtcct ggagagagat gtttttagaa 420
cggcctcgtg ttcggtttga tggcgtgtat atcagtaaaa ccacatatat tcgtcaaggg 480
gaacagtctc ttgatggttt ctatagagcc tggcaccaag tggaatatta caggtacata 540
agattctttc ctgatggcca tgtgatgatg ttgacaaccc ctgaagagcc tcagtccatt 600
gttccacgtt taagaactag gaataccagg actgatgcaa ttctactggg tcaactatgc 660
ttgtcacaaag acacagacaa tcagacccaa gtatttgctg taataactaa gaaaaaagaa 720
gaaaaaccac ttgactataa atacagatat tttcgtcgtg tccctgtaca agaagcagat 780
cagagttttc atgtggggct acagctatgt tccagtgggc accagagggt caacaaactc 840
atctggatac atcattcttg tcacattact taaaaatcaa ctggtgagac tgcagtcagt 900
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<210> 58
<211> 327

<212> PRT

<213> Homo sapiens

<400> 58

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Pro	Asp	Gly	Asp	Gly	Val	Gly	Asn	Ser	Tyr	Ile	Glu	Asp	Asn	Asp	Asp	
		20					25						30			
Asp	Ser	Lys	Met	Ala	Asp	Leu	Leu	Ser	Tyr	Phe	Gln	Gln	Gln	Leu	Thr	
		35				40						45				
Phe	Gln	Glu	Ser	Val	Leu	Lys	Leu	Cys	Gln	Pro	Glu	Leu	Glu	Ser	Ser	
	50					55					60					
Gln	Ile	His	Ile	Ser	Val	Leu	Pro	Met	Glu	Val	Leu	Met	Tyr	Ile	Phe	
65					70					75					80	
					85					90					95	
Ser	Leu	Val	Cys	Arg	Gly	Phe	Tyr	Ile	Cys	Ala	Arg	Asp	Pro	Glu	Ile	
			100					105					110			
Trp	Arg	Leu	Ala	Cys	Leu	Lys	Val	Trp	Gly	Arg	Ser	Cys	Ile	Lys	Leu	
		115					120					125				
Val	Pro	Tyr	Thr	Ser	Trp	Arg	Glu	Met	Phe	Leu	Glu	Arg	Pro	Arg	Val	
	130					135					140					
Arg	Phe	Asp	Gly	Val	Tyr	Ile	Ser	Lys	Thr	Thr	Tyr	Ile	Arg	Gln	Gly	
145					150					155					160	
Glu	Gln	Ser	Leu	Asp	Gly	Phe	Tyr	Arg	Ala	Trp	His	Gln	Val	Glu	Tyr	
				165					170					175		
Tyr	Arg	Tyr	Ile	Arg	Phe	Phe	Pro	Asp	Gly	His	Val	Met	Met	Leu	Thr	
			180					185					190			
Thr	Pro	Glu	Glu	Pro	Gln	Ser	Ile	Val	Pro	Arg	Leu	Arg	Thr	Arg	Asn	
		195					200					205				
Thr	Arg	Thr	Asp	Ala	Ile	Leu	Leu	Gly	His	Tyr	Arg	Leu	Ser	Gln	Asp	
	210					215					220					
Thr	Asp	Asn	Gln	Thr	Lys	Val	Phe	Ala	Val	Ile	Thr	Lys	Lys	Lys	Glu	
225					230					235					240	
Glu	Lys	Pro	Leu	Asp	Tyr	Lys	Tyr	Arg	Tyr	Phe	Arg	Arg	Val	Pro	Val	
				245					250					255		
Gln	Glu	Ala	Asp	Gln	Ser	Phe	His	Val	Gly	Leu	Gln	Leu	Cys	Ser	Ser	
			260					265					270			
Gly	His	Gln	Arg	Phe	Asn	Lys	Leu	Ile	Trp	Ile	His	His	Ser	Cys	His	
	275						280					285				
Ile	Thr	Tyr	Lys	Ser	Thr	Gly	Glu	Thr	Ala	Val	Ser	Ala	Phe	Glu	Ile	
	290					295					300					
Asp	Lys	Met	Tyr	Thr	Pro	Leu	Phe	Phe	Ala	Arg	Val	Arg	Ser	Tyr	Thr	

305

310

315

320

Ala Phe Ser Glu Arg Pro Leu
325

<210> 59

<211> 765

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> all n positions

<223> n=a, c, g or t

<400> 59

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catgcaaadc catatgttct ccgagctttt gaagacttta gaaagtcttc tgagcaagat 120
gattctgtag agcgagatat aattttacag tgtagagaag gtgaacttgt acttccggat 180
ttggaaaaag atgatatgat tgttcgccga atcccagcac agaagaaaga agtgccgctg 240
tctggggccc cagatagata ccacccagtc ccttttcccg aaccctggac tcttcctcca 300
gaaattcaag caaaatttct ctgtgtactt gaaaggacat gcccatccaa agaaaaaagt 360
aatagctgta gaattattagtc tccttcatat cggcagaaga aagatgacat gctgacacgt 420
aagattcagt cctggaaact gggaactacc gtgcctccca tcagtttcac ncctggcccc 480
tgcatgagg ctgacttgaa gagatgggag gccatccggg aggccagcag actcaggcac 540
aagaaaaggc tgatggtgga gagactcttt caaaagattt atggtgagaa tgggagtaag 600
tccatgagtg atgtcagcgc agaagatggt caaaacttgc gtcagctgcg ttacgaggag 660
atgcagaaaa taaaatcaca attaaaagaa caagatcaga aatggcagga tgaccttgca 720
aaatggaaaag atcgtcgaaa aagttacact tcagatctgc agaag 765
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<210> 60

<211> 255

<212> PRT

<213> Homo sapiens

<400> 60

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Thr Gly Ala Phe His Ala Asn Pro Tyr Val Leu Arg Ala Phe Glu Asp
      20              25              30

Phe Arg Lys Phe Ser Glu Gln Asp Asp Ser Val Glu Arg Asp Ile Ile
      35              40              45

Leu Gln Cys Arg Glu Gly Glu Leu Val Leu Pro Asp Leu Glu Lys Asp
      50              55              60

Asp Met Ile Val Arg Arg Ile Pro Ala Gln Lys Lys Glu Val Pro Leu
      65              70              75              80

Ser Gly Ala Pro Asp Arg Tyr His Pro Val Pro Phe Pro Glu Pro Trp
      85              90              95

Thr Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg
      100             105             110

Thr Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro
      115             120             125
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Ser Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser
 130 135 140
 Trp Lys Leu Gly Thr Thr Val Pro Pro Ile Ser Phe Thr Pro Gly Pro
 145 150 155 160
 Cys Ser Glu Ala Asp Leu Lys Arg Trp Glu Ala Ile Arg Glu Ala Ser
 165 170 175
 Arg Leu Arg His Lys Lys Arg Leu Met Val Glu Arg Leu Phe Gln Lys
 180 185 190
 Ile Tyr Gly Glu Asn Gly Ser Lys Ser Met Ser Asp Val Ser Ala Glu
 195 200 205
 Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile
 210 215 220
 Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala
 225 230 235 240
 Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys
 245 250 255

<210> 61
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 61
 Leu Pro Pro Glu Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr
 1 5 10 15
 Asp Leu Cys Leu Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu
 20 25 30
 Leu Leu Trp Gln
 35

<210> 62
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 62
 Leu Pro Gly Glu Val Leu Glu Tyr Ile Leu Cys Cys Gly Ser Leu Thr
 1 5 10 15
 Ala Ala Asp Ile Gly Arg Val Ser Ser Thr Cys Arg Arg Leu Arg Glu
 20 25 30
 Leu Cys Gln Ser Ser Gly Lys Val Trp Lys
 35 40

<210> 63
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 63

Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala Lys Ala
1 5 10 15

Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys Val Arg
20 25 30

Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile
35 40

<210> 64

<211> 39

<212> PRT

<213> Homo sapiens

<400> 64

Leu Pro Asp Glu Val Val Leu Lys Ile Phe Ser Tyr Leu Leu Glu Gln
1 5 10 15

Asp Leu Cys Arg Ala Ala Cys Val Cys Lys Arg Phe Ser Glu Leu Ala
20 25 30

Asn Asp Pro Asn Leu Trp Lys
35

<210> 65

<211> 41

<212> PRT

<213> Homo sapiens

<400> 65

Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala Tyr Leu His Leu Pro
1 5 10 15

Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala Trp Tyr Glu Leu Ile
20 25 30

Leu Ser Leu Asp Ser Thr Arg Trp Arg
35 40

<210> 66

<211> 39

<212> PRT

<213> Homo sapiens

<400> 66

Leu Pro Thr Asp Pro Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg
1 5 10 15

Asp Leu Ile Asn Cys Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser
20 25 30

Ser His Asp Pro Leu Trp Arg
35

<210> 67

<211> 40
<212> PRT
<213> Homo sapiens

<400> 67
Leu Pro Glu Pro Leu Leu Leu Arg Val Leu Ala Ala Leu Pro Ala Ala
1 5 10 15
Glu Leu Val Gln Ala Cys Arg Leu Val Cys Leu Arg Trp Lys Glu Leu
20 25 30
Val Asp Gly Ala Pro Leu Trp Leu
35 40

<210> 68
<211> 40
<212> PRT
<213> Homo sapiens

<400> 68
Leu Phe Pro Pro Glu Leu Val Glu His Ile Ile Ser Phe Leu Pro Val
1 5 10 15
Arg Asp Leu Val Ala Leu Gly Gln Thr Cys Arg Tyr Phe His Glu Val
20 25 30
Cys Asp Gly Glu Gly Val Trp Arg
35 40

<210> 69
<211> 44
<212> PRT
<213> Homo sapiens

<400> 69
Leu Pro Glu Val Leu Leu Leu His Met Cys Ser Tyr Leu Asp Met Arg
1 5 10 15
Ala Leu Gly Arg Leu Ala Gln Val Tyr Arg Trp Leu Trp His Phe Thr
20 25 30
Asn Cys Asp Leu Leu Arg Arg Gln Ile Ala Trp Ala
35 40

<210> 70
<211> 40
<212> PRT
<213> Homo sapiens

<400> 70
Leu Pro Leu His Met Leu Asn Asn Ile Leu Tyr Arg Phe Ser Asp Gly
1 5 10 15
Trp Asp Ile Ile Thr Leu Gly Gln Val Thr Pro Thr Leu Tyr Met Leu
20 25 30
Ser Glu Asp Arg Gln Leu Trp Lys
35 40

<210> 71
<211> 39
<212> PRT
<213> Homo sapiens

<400> 71
Leu Pro Asp His Ser Met Val Gln Ile Phe Ser Phe Leu Pro Thr Asn
1 5 10 15
Gln Leu Cys Arg Cys Ala Arg Val Cys Arg Arg Trp Tyr Asn Leu Ala
20 25 30
Trp Asp Pro Arg Leu Trp Arg
35

<210> 72
<211> 44
<212> PRT
<213> Homo sapiens

<400> 72
Ile Pro Leu Glu Ile Leu Val Gln Ile Phe Gly Leu Leu Val Ala Ala
1 5 10 15
Asp Gly Pro Met Pro Phe Leu Gly Arg Ala Ala Arg Val Cys Arg Arg
20 25 30
Trp Gln Glu Ala Ala Ser Gln Pro Ala Leu Trp His
35 40

<210> 73
<211> 39
<212> PRT
<213> Homo sapiens

<400> 73
Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu Asn Pro Gln
1 5 10 15
Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser Gln Leu Thr
20 25 30
Lys Thr Gly Ser Leu Trp Lys
35

<210> 74
<211> 39
<212> PRT
<213> Homo sapiens

<400> 74
Leu Pro Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val
1 5 10 15
Thr Leu Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala
20 25 30

Leu Asp Gly Ser Asn Trp Gln
35

<210> 75

<211> 48

<212> PRT

<213> Homo sapiens

<400> 75

Leu Pro Tyr Glu Leu Ile Gln Leu Ile Leu Asn His Leu Thr Leu Pro
1 5 10 15

Asp Leu Cys Arg Leu Ala Gln Thr Cys Lys Leu Leu Ser Gln His Cys
20 25 30

Cys Asp Pro Leu Gln Tyr Ile His Leu Asn Leu Gln Pro Tyr Trp Ala
35 40 45

<210> 76

<211> 44

<212> PRT

<213> Homo sapiens

<400> 76

Leu Pro Met Glu Val Leu Met Tyr Ile Phe Arg Trp Val Val Ser Ser
1 5 10 15

Asp Leu Asp Leu Arg Ser Leu Glu Gln Leu Ser Leu Val Cys Arg Gly
20 25 30

Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile Trp Arg
35 40

<210> 77

<211> 49

<212> PRT

<213> Homo sapiens

<400> 77

Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg Thr
1 5 10 15

Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro Ser
20 25 30

Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser Trp
35 40 45

Lys

<210> 78

<211> 39

<212> PRT

<213> Homo sapiens

<400> 78

Leu Pro His His Val Val Leu Gln Ile Phe Gln Tyr Leu Pro Leu Leu
1 5 10 15

Asp Arg Ala Cys Ala Ser Ser Val Cys Arg Arg Trp Asn Glu Val Phe
20 25 30

His Ile Ser Asp Leu Trp Arg
35

<210> 79

<211> 43

<212> PRT

<213> Homo sapiens

<400> 79

Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile Ser Ala Leu
1 5 10 15

Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys Gly Ser Trp
20 25 30

Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala
35 40

<210> 80

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 80

agtagtaaca aaggtcaaag acagttgact gtatcgtcga ggatgccttc aattaagtt 59

<210> 81

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 81

gcgggttactt acttagagct cgacgtctta cttacttagc tcacttctct tcacacca 58

<210> 82

<211> 12

<212> PRT

<213> Homo sapiens

<400> 82

Cys Asp Gly Glu Lys Asp Thr Tyr Ser Tyr Leu Ala
1 5 10

<210> 83
<211> 25
<212> PRT
<213> Homo sapiens

<400> 83
Cys Glu Ser Ser Phe Ser Leu Asn Met Asn Phe Ser Ser Lys Arg Thr
1 5 10 15
Lys Phe Lys Ile Thr Thr Ser Met Gln
20 25

<210> 84
<211> 12
<212> PRT
<213> Homo sapiens

<400> 84
Cys Glu Glu Ala Gln Val Arg Lys Glu Asn Gln Trp
1 5 10

<210> 85
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> Phosphorylation
<222> 8
<223> Phosothreonine

<400> 85
Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly Leu Arg Arg
1 5 10 15
Arg Gln Thr

<210> 86
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 86
cctgggggat gttctca

17

<210> 87
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 87

ggcttccggg catttag

17

<210> 88

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 88

catctggcac gattcca

17

<210> 89

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 89

ccgctcatcg tatgaca

17

<210> 90

<211> 19

<212> PRT

<213> Homo sapiens

<220>

<221> Phosphorylation

<222> 8

<223> Phosotyrosine

<400> 90

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Pro His Ser